

## Supplementary Text

### Simulation

We performed the fine-mapping on a range of simulated phenotypes to test whether the methods will reach 95% coverage of the CpG-SNP under ideal conditions. Using the UK10K dataset ([UK10K Consortium, 2015](#)) (n=3781, filtered on  $MAF \geq 0.01$ ) we simulated phenotypes similar to mQTL with a CpG-SNP (large effect, single causal variant), and for three different heritabilities  $h^2 = 0.05, 0.1, 0.2$  at the lower end of the distribution in our analysis (Figure S1). The causal variant was randomly sampled from the genome with  $MAF \geq 0.05$ . This was repeated for a randomly sampled subset of the individuals, to match the sample size of the LBC dataset (n=1366). The simulations were replicated 1000 times for each heritability and sample size. All of the fine-mapping methods were performed chromosome-wide to avoid making any assumptions about the LD structure.

All of the methods ([Davidson, R and MacKinnon, JG, 1981](#); [Servin and Stephens, 2007](#); [Zhou et al., 2013](#)) successfully capture the causal variant approximately 95% of the time (Table S3), confirming that the fine-mapping methods do work as expected on this type of trait (single causal variant with large effect size). The three methods performed similarly in terms of credible set sizes, only differing in median credible set size by a maximum of 1 SNP. However, of the three methods the J-test is the most computationally efficient and most readily scalable to larger sample sizes. The three methods were consistent in capturing the causal SNP in the credible set for all simulations (Figure S5).

### Non-reference Discordance rate

The non-reference discordance rate (NRD) ([DePristo et al., 2011](#)) between imputed and sequenced SNPs was computed for the common SNPs ( $MAF > 0.1$ ) (Table S2). The mean NRD between genotyped SNPs and sequenced SNPs was 0.4%, this will be a combination of both errors in genotyping and sequencing. The mean NRD between sequenced SNPs and HRC imputed SNPs was half that of the mean NRD between sequenced SNPs and 1000G imputed SNPs, 1.6% and 3.2% respectively, this is an average of more than 3 errors per 100 minor alleles when using the 1000G as a reference panel for imputation.

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